



09/765,061

03CO

200-Seq

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 1

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6749 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic) human

(ix) FEATURE:

- (A) NAME/KEY: AIPL1 gene
- (B) LOCATION: 17p13.1
- (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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PATENT & TRADE MARK OFFICE

11/25/01

DIVISION

RECEIVED

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA Baboon

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 gene
- (B) LOCATION:
- (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA Chimpanzee

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 gene
- (B) LOCATION:
- (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA Cow

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 gene
- (B) LOCATION:
- (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA Dog

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 gene
- (B) LOCATION:
- (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1075 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA mouse
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 gene
  - (B) LOCATION:
  - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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atggacgtct ctctactcct caatgtggag ggtgtcaaga agaccattct gcatgggggg 60
acaggagagc tccccaactt catcactggc tccagagtga cctttcattt ccgaacaatg 120
aagtgtgatg aagaacgcac ggtgatcgat gacagcaagc aggtgggcca gcccatgagc 180
atcatcatcg gcaacatggt caagctggag gtgtgggaga cgctgctgac ctccatgcgg 240
ctgggcgagg tggctgagtt ctggtgcgac accattcaca caggggtcta ccctatgttg 300
tcccgcagtc tgcggcaggt ggctgagggc aaggacccca caagctggca tgtgcacacg 360
tgcggggttg ccaacatggt tgcataccac acgctgggct acgaggacct ggatgagctg 420
cagaaagagc cacagcctct tgtcttcctg tatgaactgt tgcaggtgga ggcccaaat 480
gagtaccaga gggagacgtg gaacctgaat aatgaagaga ggatgcaggc ggtacctctt 540
cttcatggag aaggcaacag gctctacaag ctgggacgct atgatcaggc cgccaccaag 600
taccaggagg ccattgtgtg cctgaggaac cttcagacca aggagaagcc ctgggaggtt 660
gagtggctga agctggagaa gatgatcaac accctgatcc tcaactactg ccagtgcctg 720
ctgaagaagg aggagtacta cgaggtgttg gagcacacca gcgacattct acgacaccac 780
ccagggatcg tgaaggccta ctatatgcgc gcacgtgctc acgcagaggt gtggaacgct 840
gaggaggcca aggcggacct ggagaaagtg ctggagttgg agccatccat gcgcaaggcg 900
gtgctcaggg aactgcggct gctggagagc cgctggcgcg acaaacagga ggaggagcgg 960
cagcgtgcc ggagcatgct gggctaggct gggctggatt ccactgagtt agactgggtt 1020
aggttgggtg ggagctgcgg gttgaaccct ggggcgaggg ctggggctat ggact 1075

```

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1179 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA Rhesus monkey
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 gene
  - (B) LOCATION:
  - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

atggatgccg ctctgctcct gaacgtggaa ggggtcaaga aaaccattct gcacggaggc 60
acgggcgagc tcccaaactt catcaccgga tcccgagtga tctttcattt ccgcaccatg 120
aaatgtgatg aggagcgcac ggtcatcgac gacagccgct aggtggacca gcccatgcac 180
atcatcatcg ggaacatggt caagctcgag gtctgggaga tcctgctcac ctccatgagg 240
gtgcacgagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatyctg 300
tcccggagcc tgcggcagat ggcccagggc aaggacccca cggagtggca cgtgcacaca 360
tgcgggctgg ccaacatggt cgcctaccac acgctgggct acgaggacct ggacgagctg 420

```

cagaaggagc	ctcagcctct	gatctttgtg	atcgagctgc	tgcaggttga	cgccccgagt	480
gattaccaga	gggagacctg	gaacctgagc	aatcatgaga	agatgaaggt	ggtgcccgtc	540
ctccacggag	agggaaatcg	gctcttcaag	ytgggccgct	acgaggaggc	ctcttccaag	600
taccaggagg	ccatcatctg	cctaaggaac	ctgcagacca	aggagaagcc	gtgggaggtg	660
cagtggctga	agctggagaa	gatgatcaac	accctgacct	tcaactactg	ccagtgcctg	720
ctgaagaagg	aggagtatta	cgaggtgctg	gagcacacca	gtgacattct	ccggcaccac	780
ccaggcatcg	tgaaggccta	ctatgtgcgt	gcccgggctc	acgcggaggt	gtggaacgag	840
gccgaggcca	aggcggacct	ccagaaagtg	ctggagctgg	agccatccat	gcagaaggcg	900
gtgcgagggg	agctgaggct	gctggagaac	cgcatggcgg	agaagcagga	ggaggagagg	960
ctgcgctgcc	ggaacatgct	gagccagggg	gccacgcagc	ctcccgcaga	gccaccggca	1020
cagcccccca	cagcaccacc	tgcagagctg	tccacagggc	cacctgcgga	cccaccggcg	1080
gagcccccca	cagcaccacc	tgcggagctg	tccacagggc	cacctgcaga	gccaccgcga	1140
gagctccccc	tgtccccagg	gcactcactg	cagcactga			1179

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1129 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA Squirrel monkey

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 gene
- (B) LOCATION:
- (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

atggatgccg	ctctgctcct	gaacgtggaa	gggggtcaaga	agaccattct	gcacggggggc	60
acgggcgagc	tcccaaattt	catcacggga	tcccgagtga	tctttcattt	ccgcaccatg	120
aaatgtgatg	aggagcggac	ggtgattgac	gacagcaggg	aggtggggcca	gcccattgcac	180
atcatcatcg	ggaacatggt	caagctggag	gtctggggaga	tcctgctcac	gtccatgcgg	240
gtgcgagagg	tggccgagtt	ctggtgcgac	accatccaca	cgggggtcta	ccccatcctg	300
tcccggagcc	tgcggcagat	ggcccagggc	aaggaccgga	cggagtggca	tgtgcacacg	360
tgcgggctgg	ccaacatggt	cgctaccac	acgctgggct	acgaggacct	ggatgagctg	420
cagaaggagc	ctcagcctct	gatctttgtg	atcgagctgc	tgcaggttga	tgccccaagt	480
gattaccaga	gggagacctg	gaacctgagc	aatcacgaga	agatgaaggt	ggtgcccgtc	540
ctccatggag	aaggaaatag	gctcttcaag	ctgggccgct	acgaggaggc	ctcttccaag	600
taccaggagg	ccatcatctg	cctaaggaac	ctgcagacca	aggagaaacc	ctgggaggtg	660
cagtggctga	agctggagaa	gatgatcaat	accctgatcc	tcaactactg	tcagtgtctg	720
ctgaagaagg	aggagtacta	cgaggtcctg	gagcatacca	gtgacattct	ccggcaccac	780
ccaggcattg	tgaaggccta	ctatgtgcgc	gcccgggctc	acgcggaggt	gtggaacgag	840
gccgaggcca	aggcggacct	ccagaaagtg	ctggagctgg	agccgtccat	gcagaaggcg	900
gtgcgagggg	agctgaggct	gctggagaac	cgcatggcgg	agaagcagga	ggaggagcgg	960
ctgcgctgcc	gcaacatgct	gagccagggg	gccacgtggt	cccccgcgga	gccaccgcga	1020
gagccacctg	cagagtcatc	cacagagcca	cccgcagagc	cacctgcaga	gccacctgca	1080
gagctaacct	tgacccccgg	gcacccacta	cagcactga			1129

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 Met79Thr Mutation
  - (B) LOCATION: 77...81
  - (D) OTHER INFORMATION: Thr 79 mutation
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

acc tcc acg cgg gtg  
Thr

15

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 Trp88X mutation
  - (B) LOCATION: 86...90
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

gag ttc tga tgc gac  
X

15

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 Val96Ile mutation
  - (B) LOCATION: 94...98
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

acg ggg atc tac ccc  
Ile

15

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 Thr124Ile mutation
  - (B) LOCATION: 122...126
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

gac ccc ata gag tgg  
ile

15

- (2) INFORMATION FOR SEQ ID NO:13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 Pro376Ser mutation
    - (B) LOCATION: 374...378
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

cca ccc tcg tcc cca  
Ser

15

- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 Gln163X mutation
    - (B) LOCATION: 161...165
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

gat tac tag agg gag  
X

15

- (2) INFORMATION FOR SEQ ID NO:15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:

(A ) NAME/KEY: AIPL1 Ala197Pro mutation  
(B) LOCATION: 195...199  
(D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

gag gag ccc tct tcc  
Lys 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A ) NAME/KEY: AIPL1 Trp278X mutation  
(B) LOCATION: 276...280  
(D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

gag gtg tga aat gag  
X 15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A ) NAME/KEY: AIPL1 IVS2-2A to G mutation  
(B) LOCATION:  
(D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

tcc cca cgg cac acg  
IVS2-SA->G 15

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A ) NAME/KEY: AIPL1 Glu262Ser mutation  
(B) LOCATION: 260...264

- (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

cac cca agt gcg cgg 15  
Ser

- (2) INFORMATION FOR SEQ ID NO:19:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 bases  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A ) NAME/KEY: AIPL1 Arg302Leu mutation  
    (B) LOCATION: 300...304  
    (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

gcg gtg ctc agg gag 15  
Leu

- (2) INFORMATION FOR SEQ ID NO:20:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 bases  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A ) NAME/KEY: AIPL1 Pro351del12 mutation  
    (B) LOCATION: Pro351  
    (D) OTHER INFORMATION: TGCAGAGCCACC deleted  
    sequence  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

g cca ccc aca gca 13  
del TGCAGAGCCACC

- (2) INFORMATION FOR SEQ ID NO:21:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 bases  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A ) NAME/KEY: AIPL1 Cys239Arg mutation  
    (B) LOCATION: 237...241  
    (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

tgc cag cgc ctg ctg  
Arg

15

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 Ala336del2 mutation
- (B) LOCATION: Ala336 2 base deletion
- (D) OTHER INFORMATION: AG deleted sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

t ccc gca gcc acc  
del AG

13

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 Cys42X mutation
- (B) LOCATION: 40...44
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

atg aaa tga gat gag  
X

15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 Leu257del9 mutation
- (B) LOCATION: Leu 257 9 base deletion
- (D) OTHER INFORMATION: CTCGGCAC deleted sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

gat att cac cca  
del CTCCGGCAC

12

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 Val33ins8 mutation
- (B) LOCATION: Val 33 8 base insertion
- (D) OTHER INFORMATION: GTGATCTT inserted sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

gac tag gtg atc ttg tga tct  
ins GTGATCTT

21

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: AIPL1 IVS1-9G to A Benign Variants/Polymorphisms
- (B) LOCATION:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ctc agt gac tag  
G->A

12

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 IVS2+66G to C Benign Variants/Polymorphisms
- (B) LOCATION:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ttt gcc ggg ctg  
G->C

12

- (2) INFORMATION FOR SEQ ID NO:28:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 IVS2-88C to T Benign Variants/Polymorphisms
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

tcc tct cag gag  
C->T

12

- (2) INFORMATION FOR SEQ ID NO:29:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 IVS2-14G to A Benign Variants/Polymorphisms
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

atc cat tta tcc  
G->A

12

- (2) INFORMATION FOR SEQ ID NO:30:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 IVS2-10A to C Benign Variants/Polymorphisms
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

cgt ttc tcc cca  
A->C

12

- (2) INFORMATION FOR SEQ ID NO:31:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 IVS3-25T to C Benign Variants/Polymorphisms
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ctg ccc cac tga  
T->C

12

- (2) INFORMATION FOR SEQ ID NO:32:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 IVS3-21T to C Benign Variants/Polymorphisms
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

cct cac cga cct  
T->C

12

- (2) INFORMATION FOR SEQ ID NO:33:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 IVS5+18G to A Benign Variants/Polymorphisms
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

agg agc gga cag  
G->A

12

- (2) INFORMATION FOR SEQ ID NO:34:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 Asp90His Benign Variants/Polymorphisms
    - (B) LOCATION: 88...91
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

tgg tgc cac acc  
His

12

- (2) INFORMATION FOR SEQ ID NO:35:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 Phe37Phe Benign Variants/Polymorphisms
    - (B) LOCATION: 36...39
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

cat ttc cgc acc  
Phe

12

- (2) INFORMATION FOR SEQ ID NO:36:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 Ser78Ser Benign Variants/Polymorphisms
    - (B) LOCATION: 77...79
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:



acc tct atg cgg  
Ser

12

- (2) INFORMATION FOR SEQ ID NO:37:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 Cys89Cys Benign Variants/Polymorphisms
    - (B) LOCATION: 88...91
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

tgg tgt gac acc  
Cys

12

- (2) INFORMATION FOR SEQ ID NO:38:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 Leu100Leu Benign Variants/Polymorphisms
    - (B) LOCATION: 99...102
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

atc ctg tcc cgg  
Leu

12

- (2) INFORMATION FOR SEQ ID NO:39:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 His172His Benign Variants/Polymorphisms
    - (B) LOCATION: 171...174
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

aat cac gag aag  
His

12

- (2) INFORMATION FOR SEQ ID NO:40:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 Pro217Pro Benign Variants/Polymorphisms
    - (B) LOCATION: 216...219
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

aag ccg tgg gag  
Pro

12

- (2) INFORMATION FOR SEQ ID NO:41:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 Asp255Asp Benign Variants/Polymorphisms
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

agt gac att ctc  
Asp

12

- (2) INFORMATION FOR SEQ ID NO:42:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA Primer
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 primer
    - (B) LOCATION:
    - (D) OTHER INFORMATION: 5' to 3' order
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

5'-aagaaaaccattctgcacgg-3'

20

- (2) INFORMATION FOR SEQ ID NO:43:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA Primer
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 primer
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

5'-tgcagctcgtccaggtcct-3'

19

- (2) INFORMATION FOR SEQ ID NO:44:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Primer DNA
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 primer
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

5'-gacacctcccttttctcc-3'

17

- (2) INFORMATION FOR SEQ ID NO:45:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Primer DNA (genomic) human
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 primer
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

5'-gctggggctgcctggctg-3'

18

- (2) INFORMATION FOR SEQ ID NO:46:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 bases

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Primer DNA (genomic) human
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 Primer
  - (B) LOCATION:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

5'-ccgagtgattaccagagga-3'

20

- (2) INFORMATION FOR SEQ ID NO:47:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Primer DNA (genomic) human
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 Primer
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

5'-tgagctccagcacctcatag-3'

20

- (2) INFORMATION FOR SEQ ID NO:48:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Primer DNA (genomic) human
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 primer
    - (B) LOCATION:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

5'-acgcagaggtgtggaatg-3'

18

- (2) INFORMATION FOR SEQ ID NO:49:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Primer DNA (genomic) human
  - (ix) FEATURE:

- (A ) NAME/KEY: AIPL1 Primer
- (B) LOCATION:
- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

5'-aaaaagtgacaccacgatc-3'

19

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA (genomic) human

(ix) FEATURE:

(A ) NAME/KEY: AIPL1 gene exon/intron donor splice site

(B) LOCATION:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGGATCCCGAgtgagtgggggccctccggagcaga

34

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A ) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site

(B) LOCATION:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

cagagtgcccggtctcggtgactagGTGATCTTTC

35

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic) human

(ix) FEATURE:

(A ) NAME/KEY: AIPL1 gene exon/intron Donor splice site

(B) LOCATION:

- (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CSACACCATCgtaagtaggcctgcgcgctgtct

35

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 bases  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic) human  
(ix) FEATURE:  
    (A ) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site  
    (B) LOCATION: 17p13.1  
    (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

gccatccatccgtttatccccacagCACACGGGGG

35

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 bases  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic) human  
(ix) FEATURE:  
    (A ) NAME/KEY: AIPL1 gene exon/intron Donor splice site  
    (B) LOCATION:  
    (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTGCTGCAGgtggggctgggggttggcagggctgg

35

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 6689 bases  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(ix) FEATURE:  
    (A ) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site  
    (B) LOCATION:  
    (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

cactgacctgcagctctggggccagGTTGATGCCC

35

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A ) NAME/KEY: AIPL1 gene exon/intron Donor splice site

(B) LOCATION:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCAGACCAAGgtcagaggccgctggccacggggtg

35

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A ) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site

(B) LOCATION:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

catggctgaccttctccctgggcagGAGAAGCCRT

35

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic) human

(ix) FEATURE:

(A ) NAME/KEY: AIPL1 gene exon/intron Donor splice site

(B) LOCATION:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CACCACCCAGgtgcgcggggctgcaggggcggaca

35

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic) human
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site
  - (B) LOCATION:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

gctggatgctccctgctccccacagGCATCGTGAA

35

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA Primer
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 gene Exon 1 Primer
  - (B) LOCATION: 240
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

5'-ggacacctcccttttctcc-3'

18

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA Primer
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 gene Exon 1 Primer
  - (B) LOCATION: 240
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

5'-gctggggctgcctggctg-3'

18

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 bases
  - (B) TYPE: nucleic acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA Primer
- (ix) FEATURE:
  - (A ) NAME/KEY: AIPL1 gene Exon 2 Primer
  - (B) LOCATION: 297
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

5'-gggccttgaacagtgtgtct-3'

20

- (2) INFORMATION FOR SEQ ID NO:63:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA Primer
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 gene Exon 2 Primer
    - (B) LOCATION: 297
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

5'-tttcccgaacacagcagc-3'

19

- (2) INFORMATION FOR SEQ ID NO:64:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA Primer
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 gene Exon 3 Primer
    - (B) LOCATION: 364
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

5'-agtgaggagcaggattc-3'

18

- (2) INFORMATION FOR SEQ ID NO:65:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA Primer
  - (ix) FEATURE:
    - (A ) NAME/KEY: AIPL1 gene Exon 3 Primer

(B) LOCATION: 364  
(D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

5'-tgcccatgatgcccgctgtc-3'

20

(2) INFORMATION FOR SEQ ID NO:66:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 bases  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA Primer  
(ix) FEATURE:  
    (A ) NAME/KEY: AIPL1 gene Exon 4 Primer  
    (B) LOCATION: 315  
    (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

5'-tttcgggtctctgatggg-3'

18

(2) INFORMATION FOR SEQ ID NO:67:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 bases  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA Primer  
(ix) FEATURE:  
    (A ) NAME/KEY: AIPL1 gene Exon 4 Primer  
    (B) LOCATION: 315  
    (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

5'-gcaggctccccagagtc-3'

17

(2) INFORMATION FOR SEQ ID NO:68:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 bases  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA Primer  
(ix) FEATURE:  
    (A ) NAME/KEY: AIPL1 gene Exon 5 Primer  
    (B) LOCATION: 279  
    (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

5'-gcagctgcctcaggtcatg-3'

19

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA Primer

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 gene Exon 5 Primer
- (B) LOCATION: 279
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

5'-gtggggtggaaagaaaag-3'

18

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA Primer

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 gene Exon 6 Primer
- (B) LOCATION: 497
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

5'-ctgggaagggagctgtag-3'

18

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA Primer

(ix) FEATURE:

- (A ) NAME/KEY: AIPL1 gene Exon 6 Primer
- (B) LOCATION: 497
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

5'-aaaagtgacaccacgatcc-3'

19

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A ) NAME/KEY: Human Aipl1

(B) LOCATION:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	Asp	Ala	Ala	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr
1				5					10					15
Ile	Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly
			20						25					30
Ser	Arg	Val	Ile	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu
			35						40					45
Arg	Thr	Val	Ile	Asp	Asp	Ser	Arg	Gln	Val	Gly	Gln	Pro	Met	His
			50						55					60
Ile	Ile	Ile	Gly	Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu
			65						70					75
Leu	Thr	Ser	Met	Arg	Val	His	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp
			80						85					90
Thr	Ile	His	Thr	Gly	Val	Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg
			95						100					105
Gln	Met	Ala	Gln	Gly	Lys	Asp	Pro	Thr	Glu	Trp	His	Val	His	Thr
			110						115					120
Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	Tyr	His	Thr	Leu	Gly	Tyr	Glu
			125						130					135
Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	Gln	Pro	Leu	Val	Phe	Val
			140						145					150
Ile	Glu	Leu	Leu	Gln	Val	Asp	Ala	Pro	Ser	Asp	Tyr	Gln	Arg	Glu
			155						160					165
Thr	Trp	Asn	Leu	Ser	Asn	His	Glu	Lys	Met	Lys	Ala	Val	Pro	Val
			170						175					180
Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly	Arg	Tyr	Glu
			185						190					195
Glu	Ala	Ser	Ser	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu	Arg	Asn
			200						205					210
Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys	Leu
			215						220					225
Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu
			230						235					240
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp
			245						250					255
Ile	Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Val	Arg
			260						265					270
Ala	Arg	Ala	His	Ala	Glu	Val	Trp	Asn	Glu	Ala	Glu	Ala	Lys	Ala
			275						280					285
Asp	Leu	Gln	Lys	Val	Leu	Glu	Leu	Glu	Pro	Ser	Met	Gln	Lys	Ala
			290						295					300
Val	Arg	Arg	Glu	Leu	Arg	Leu	Leu	Glu	Asn	Arg	Met	Ala	Glu	Lys
			305						310					315
Gln	Glu	Glu	Glu	Arg	Leu	Xxx	Cys	Arg	Asn	Met	Leu	Ser	Gln	Gly

	320		325		330
Ala Thr Gln Pro	Pro Ala Glu Pro Pro	Thr Glu Pro Pro	Ala Gln		
	335		340		345
Ser Ser Thr Glu	Pro Pro Ala Glu Pro	Pro Thr Ala Pro	Ser Ala		
	350		355		360
Glu Leu Ser Ala	Gly Pro Pro Ala Glu	Pro Ala Thr Glu	Pro Pro		
	365		370		375
Pro Ser Pro Gly	His Ser Leu Gln His				
	380		383		

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A ) NAME/KEY: Chimpanzee Aipl1
- (B) LOCATION:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met	Asp	Ala	Ala	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr
1				5					10					15
Ile	Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly
			20						25					30
Ser	Arg	Val	Ile	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu
			35						40					45
Arg	Thr	Val	Ile	Asp	Asp	Ser	Arg	Gln	Val	Gly	Gln	Pro	Met	His
			50						55					60
Ile	Ile	Ile	Gly	Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu
			65						70					75
Leu	Thr	Ser	Met	Arg	Val	His	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp
			80						85					90
Thr	Ile	His	Thr	Gly	Val	Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg
			95						100					105
Gln	Met	Ala	Gln	Gly	Lys	Asp	Pro	Thr	Glu	Trp	His	Val	His	Thr
			110						115					120
Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	Tyr	His	Thr	Leu	Gly	Tyr	Glu
			125						130					135
Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	Gln	Pro	Leu	Val	Phe	Val
			140						145					150
Ile	Glu	Leu	Leu	Gln	Val	Asp	Ala	Pro	Ser	Asp	Tyr	Gln	Arg	Glu
			155						160					165
Thr	Trp	Asn	Leu	Ser	Asn	His	Glu	Lys	Met	Lys	Ala	Val	Pro	Val
			170						175					180
Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly	Arg	Tyr	Glu
			185						190					195
Glu	Ala	Ser	Ser	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu	Arg	Asn
			200						205					210

Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys	Leu	215	220	225
Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu	230	235	240
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp	245	250	255
Ile	Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Val	Arg	260	265	270
Ala	Arg	Ala	His	Ala	Glu	Val	Trp	Asn	Glu	Ala	Glu	Ala	Lys	Ala	275	280	285
Asp	Leu	Arg	Lys	Val	Leu	Glu	Leu	Glu	Pro	Ser	Met	Gln	Lys	Ala	290	295	300
Val	Arg	Arg	Glu	Leu	Arg	Leu	Leu	Glu	Asn	Arg	Met	Ala	Glu	Lys	305	310	315
Gln	Glu	Glu	Glu	Arg	Leu	Arg	Cys	Arg	Asn	Met	Leu	Ser	Gln	Gly	320	325	330
Ala	Thr	Gln	Pro	Pro	Ala	Glu	Pro	Pro	Thr	Glu	Pro	Pro	Ala	Gln	335	340	345
Ser	Ser	Thr	Glu	Pro	Pro	Ala	Glu	Pro	Pro	Pro	Ala	Pro	Ser	Ala	350	355	360
Glu	Leu	Ser	Ala	Gly	Pro	Pro	Ala	Glu	Thr	Ala	Thr	Glu	Pro	Pro	365	370	375
Pro	Ser	Pro	Gly	His	Ser	Leu	Gln	His							365	369	

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A ) NAME/KEY: Baboon Aipl1

(B) LOCATION:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met	Asp	Ala	Ala	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr	1	5	10	15
Ile	Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly	20	25	30	
Ser	Arg	Val	Ile	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu	35	40	45	
Arg	Thr	Val	Ile	Asp	Asp	Ser	Arg	Gln	Val	Asp	Gln	Pro	Met	His	50	55	60	
Ile	Ile	Ile	Gly	Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	65	70	75	
Leu	Thr	Ser	Met	Arg	Val	His	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	80	85	90	
Thr	Ile	His	Thr	Gly	Val	Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg				

				95					100					105
Gln	Met	Ala	Gln	Gly	Lys	Asp	Pro	Thr	Glu	Trp	His	Val	His	Thr
				110					115					120
Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	Tyr	His	Thr	Leu	Gly	Tyr	Glu
				125					130					135
Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	Gln	Pro	Leu	Ile	Phe	Val
				140					145					150
Ile	Glu	Leu	Leu	Gln	Val	Asp	Ala	Pro	Ser	Asp	Tyr	Gln	Arg	Glu
				155					160					165
Thr	Trp	Asn	Leu	Ser	Asn	His	Glu	Lys	Met	Lys	Val	Val	Pro	Val
				170					175					180
Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly	Arg	Tyr	Glu
				185					190					195
Glu	Ala	Ser	Ser	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu	Arg	Asn
				200					205					210
Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys	Leu
				215					220					225
Glu	Lys	Met	Ile	Asn	Thr	Leu	Thr	Leu	Asn	Tyr	Cys	Gln	Cys	Leu
				230					235					240
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp
				245					250					255
Ile	Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Val	Arg
				260					265					270
Ala	Arg	Ala	His	Ala	Glu	Val	Trp	Asn	Glu	Ala	Glu	Ala	Lys	Ala
				275					280					285
Asp	Leu	Gln	Lys	Val	Leu	Glu	Leu	Glu	Pro	Ser	Met	Gln	Lys	Ala
				290					295					300
Val	Arg	Arg	Glu	Leu	Arg	Leu	Leu	Glu	Asn	Arg	Met	Ala	Glu	Lys
				305					310					315
Gln	Glu	Glu	Glu	Arg	Leu	Arg	Cys	Arg	Asn	Met	Leu	Ser	Gln	Gly
				320					325					330
Ala	Thr	Gln	Pro	Pro	Thr	Glu	Pro	Pro	Ala	Glu	Pro	His	Thr	Ala
				335					340					345
Pro	Pro	Ala	Glu	Leu	Ser	Thr	Gly	Pro	Pro	Ala	Glu	Pro	Pro	Ala
				350					355					360
Glu	Leu	Pro	Leu	Ser	Pro	Gly	His	Ser	Leu	Gln	His			
				365					370			372		

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A ) NAME/KEY: Cow Aipl1

(B) LOCATION:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met	Asp	Ala	Thr	Leu	Leu	Leu	Asn	Val	Glu	Gly	Ile	Lys	Lys	Thr	1	5	10	15
Ile	Leu	His	Gly	Gly	Thr	Gly	Asp	Leu	Pro	Asn	Phe	Ile	Thr	Gly	20	25	30	
Ala	Arg	Val	Thr	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu	35	40	45	
Arg	Thr	Val	Ile	Asp	Asp	Ser	Lys	Gln	Val	Gly	His	Pro	Met	His	50	55	60	
Ile	Ile	Ile	Gly	Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	65	70	75	
Leu	Thr	Ser	Met	Arg	Val	Ser	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	80	85	90	
Thr	Ile	His	Thr	Gly	Val	Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg	95	100	105	
Gln	Met	Ala	Glu	Gly	Lys	Asp	Pro	Thr	Glu	Trp	His	Val	His	Thr	110	115	120	
Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	Tyr	His	Thr	Leu	Gly	Tyr	Glu	125	130	135	
Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	Gln	Pro	Leu	Ile	Phe	Ile	140	145	150	
Ile	Glu	Leu	Leu	Gln	Val	Glu	Ala	Pro	Ser	Gln	Tyr	Gln	Arg	Glu	155	160	165	
Thr	Trp	Asn	Leu	Asn	Asn	Gln	Glu	Lys	Met	Gln	Ala	Val	Pro	Ile	170	175	180	
Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly	Arg	Tyr	Glu	185	190	195	
Glu	Ala	Ser	Asn	Lys	Tyr	Gln	Glu	Ala	Ile	Val	Cys	Leu	Arg	Asn	200	205	210	
Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys	Leu	215	220	225	
Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu	230	235	240	
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp	245	250	255	
Ile	Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Val	Arg	260	265	270	
Ala	Arg	Ala	His	Ala	Glu	Val	Trp	Asn	Glu	Ala	Glu	Ala	Lys	Ala	275	280	285	
Asp	Leu	Glu	Lys	Val	Leu	Glu	Leu	Glu	Pro	Ser	Met	Arg	Lys	Ala	290	295	300	
Val	Gln	Arg	Glu	Leu	Arg	Leu	Leu	Glu	Asn	Arg	Leu	Glu	Glu	Lys	305	310	315	
Arg	Glu	Glu	Glu	Arg	Leu	Arg	Cys	Arg	Asn	Met	Leu	Gly			320	325	328	

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: protein  
 (ix) FEATURE:  
     (A ) NAME/KEY: Mouse Aipl1  
     (B) LOCATION:  
     (D) OTHER INFORMATION:  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Asp	Val	Ser	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr
1				5					10					15
Ile	Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly
				20					25					30
Ser	Arg	Val	Thr	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu
				35					40					45
Arg	Thr	Val	Ile	Asp	Asp	Ser	Lys	Gln	Val	Gly	Gln	Pro	Met	Ser
				50					55					60
Ile	Ile	Ile	Gly	Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Thr	Leu
				65					70					75
Leu	Thr	Ser	Met	Arg	Leu	Gly	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp
				80					85					90
Thr	Ile	His	Thr	Gly	Val	Tyr	Pro	Met	Leu	Ser	Arg	Ser	Leu	Arg
				95					100					105
Gln	Val	Ala	Glu	Gly	Lys	Asp	Pro	Thr	Ser	Trp	His	Val	His	Thr
				110					115					120
Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	Tyr	His	Thr	Leu	Gly	Tyr	Glu
				125					130					135
Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	Gln	Pro	Leu	Val	Phe	Leu
				140					145					150
Tyr	Glu	Leu	Leu	Gln	Val	Glu	Ala	Pro	Asn	Glu	Tyr	Gln	Arg	Glu
				155					160					165
Thr	Trp	Asn	Leu	Asn	Asn	Glu	Glu	Arg	Met	Gln	Ala	Val	Pro	Leu
				170					175					180
Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Tyr	Lys	Leu	Gly	Arg	Tyr	Asp
				185					190					195
Gln	Ala	Ala	Thr	Lys	Tyr	Gln	Glu	Ala	Ile	Val	Cys	Leu	Arg	Asn
				200					205					210
Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Glu	Trp	Leu	Lys	Leu
				215					220					225
Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu
				230					235					240
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp
				245					250					255
Ile	Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Met	Arg
				260					265					270
Ala	Arg	Ala	His	Ala	Glu	Val	Trp	Asn	Ala	Glu	Glu	Ala	Lys	Ala
				275					280					285
Asp	Leu	Glu	Lys	Val	Leu	Glu	Leu	Glu	Pro	Ser	Met	Arg	Lys	Ala
				290					295					300
Val	Leu	Arg	Glu	Leu	Arg	Leu	Leu	Glu	Ser	Arg	Leu	Ala	Asp	Lys
				305					310					315
Gln	Glu	Glu	Glu	Arg	Gln	Arg	Cys	Arg	Ser	Met	Leu	Gly		

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

(A ) NAME/KEY: Rhesus Monkey Aipl1

(B) LOCATION:

(D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met	Asp	Ala	Ala	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr	1	5	10	15
Ile	Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly	20	25	30	35
Ser	Arg	Val	Ile	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu	40	45	50	55
Arg	Thr	Val	Ile	Asp	Asp	Ser	Arg	Gln	Val	Asp	Gln	Pro	Met	His	60	65	70	75
Ile	Ile	Ile	Gly	Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	80	85	90	95
Leu	Thr	Ser	Met	Arg	Val	His	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	100	105	110	115
Thr	Ile	His	Thr	Gly	Val	Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg	120	125	130	135
Gln	Met	Ala	Gln	Gly	Lys	Asp	Pro	Thr	Glu	Trp	His	Val	His	Thr	140	145	150	155
Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	Tyr	His	Thr	Leu	Gly	Tyr	Glu	160	165	170	175
Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	Gln	Pro	Leu	Ile	Phe	Val	180	185	190	195
Ile	Glu	Leu	Leu	Gln	Val	Asp	Ala	Pro	Ser	Asp	Tyr	Gln	Arg	Glu	200	205	210	215
Thr	Trp	Asn	Leu	Ser	Asn	His	Glu	Lys	Met	Lys	Val	Val	Pro	Val	220	225	230	235
Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly	Arg	Tyr	Glu	240	245	250	255
Glu	Ala	Ser	Ser	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu	Arg	Asn	260	265	270	

Ala	Arg	Ala	His	Ala	Glu	Val	Trp	Asn	Glu	Ala	Glu	Ala	Lys	Ala	275	280	285
Asp	Leu	Gln	Lys	Val	Leu	Glu	Leu	Glu	Pro	Ser	Met	Gln	Lys	Ala	290	295	300
Val	Arg	Arg	Glu	Leu	Arg	Leu	Leu	Glu	Asn	Arg	Met	Ala	Glu	Lys	305	310	315
Gln	Glu	Glu	Glu	Arg	Leu	Arg	Cys	Arg	Asn	Met	Leu	Ser	Gln	Gly	320	325	330
Ala	Thr	Gln	Pro	Pro	Ala	Glu	Pro	Pro	Ala	Gln	Pro	Pro	Thr	Ala	335	340	345
Pro	Pro	Ala	Glu	Leu	Ser	Thr	Gly	Pro	Pro	Ala	Asp	Pro	Pro	Ala	350	355	360
Glu	Pro	Pro	Thr	Ala	Pro	Pro	Ala	Glu	Leu	Ser	Thr	Gly	Pro	Pro	365	370	375
Ala	Glu	Pro	Pro	Ala	Glu	Leu	Pro	Leu	Ser	Pro	Gly	His	Ser	Leu	380	385	390
Gln	His														392		

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A ) NAME/KEY: Squirrel Monkey Aipl1
- (B) LOCATION:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Asp	Ala	Ala	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr	1	5	10	15
Ile	Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly	20	25	30	35
Ser	Arg	Val	Ile	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu	40	45	50	55
Arg	Thr	Val	Ile	Asp	Asp	Ser	Arg	Glu	Val	Gly	Gln	Pro	Met	His	60	65	70	75
Ile	Ile	Ile	Gly	Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	80	85	90	95
Leu	Thr	Ser	Met	Arg	Val	Arg	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	100	105	110	115
Thr	Ile	His	Thr	Gly	Val	Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg	120	125	130	135
Gln	Met	Ala	Gln	Gly	Lys	Asp	Pro	Thr	Glu	Trp	His	Val	His	Thr	140	145	150	155
Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	Tyr	His	Thr	Leu	Gly	Tyr	Glu	160	165	170	175
Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	Gln	Pro	Leu	Ile	Phe	Val	180	185	190	195

Ile Glu Leu Leu	140		145		150
Gln Val Asp Ala Pro		Ser Asp Tyr Gln Arg	Glu		
	155		160		165
Thr Trp Asn Leu		Ser Asn His Glu Lys	Met Lys Val Val Pro	Val	
	170		175		180
Leu His Gly Glu		Gly Asn Arg Leu Phe	Lys Leu Gly Arg Tyr	Glu	
	185		190		195
Glu Ala Ser Ser		Lys Tyr Gln Glu Ala	Ile Ile Cys Leu Arg	Asn	
	200		205		210
Leu Gln Thr Lys		Glu Lys Pro Trp Glu	Val Gln Trp Leu Lys	Leu	
	215		220		225
Glu Lys Met Ile		Asn Thr Leu Ile Leu	Asn Tyr Cys Gln Cys	Leu	
	230		235		240
Leu Lys Lys Glu		Glu Tyr Tyr Glu Val	Leu Glu His Thr Ser	Asp	
	245		250		255
Ile Leu Arg His		His Pro Gly Ile Val	Lys Ala Tyr Tyr Val	Arg	
	260		265		270
Ala Arg Ala His		Ala Glu Val Trp Asn	Glu Ala Glu Ala Lys	Ala	
	275		280		285
Asp Leu Gln Lys		Val Leu Glu Leu Glu	Pro Ser Met Gln Lys	Ala	
	290		295		300
Val Arg Arg Glu		Leu Arg Leu Leu Glu	Asn Arg Met Ala Glu	Lys	
	305		310		315
Gln Glu Glu Glu		Arg Leu Arg Cys Arg	Asn Met Leu Ser Gln	Gly	
	320		325		330
Ala Thr Trp Ser		Pro Ala Glu Pro Pro	Ala Glu Pro Pro Ala	Glu	
	335		340		345
Ser Ser Thr Glu		Pro Pro Ala Glu Pro	Pro Ala Glu Pro Pro	Ala	
	350		355		360
Glu Leu Thr Leu		Thr Pro Gly His Pro	Leu Gln His		
	365		370	372	